



# SEQUENCE LISTING

<110> Gordon-Kamm, William  
Lowe, Keith  
Sun, Yuejin  
Dilkes, Brian  
Larkins, Brian

<120> Cell Cycle Nucleic Acids, Polypeptides,  
and Uses Thereof

<130> 1146

<160> 6

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<210> 1

<211> 1372

<212> DNA

<213> zea mays

<220>

<221> CDS

<222> (134)...(902)

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ggcgttgcgt cag atg ggg aag tac atg cgc aag tgc agg ggc gcc gca      169
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ggc gcg gag gtc gcc gcc gtc gag gtt acg cag gtc gtc ggc gtc cgg      217
Gly Ala Glu Val Ala Ala Val Glu Val Thr Gln Val Val Gly Val Arg
          15              20              25

acg agg tcc agg tcc gcg gcg gcg acc ggc ggt gtc gcg aag gtc gcc      265
Thr Arg Ser Arg Ser Ala Ala Ala Thr Gly Gly Val Ala Lys Val Ala
          30              35              40

ccg agg agg aag agg gcg ccg gcg ggg gag cct gct gcc gcc gtg agc      313
Pro Arg Arg Lys Arg Ala Pro Ala Gly Glu Pro Ala Ala Ala Val Ser
          45              50              55              60

gct ggt ggg gac ggc gga agc tgc tac atc cac ctg cgt agc cgc atg      361
Ala Gly Gly Asp Gly Gly Ser Cys Tyr Ile His Leu Arg Ser Arg Met
          65              70              75

ctg ttc atg gca ccg cct cag ccg cag ccg tcg gtt gac tcg gtt ccg      409
Leu Phe Met Ala Pro Pro Gln Pro Gln Pro Ser Val Asp Ser Val Pro
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acc ccg gtg gag gct gct gat ggc gct gca gga cag cag ggc gcg gcg      457

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Thr	Pro	Val	Glu	Ala	Ala	Asp	Gly	Ala	Ala	Gly	Gln	Gln	Gly	Ala	Ala		
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Leu	Gly	Leu	Gly	Gly	Gln	Arg	Gly	Ser	His	Thr	Cys	Arg	Ser	Tyr	Asp		
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Ser	Asn	Ser	Gly	Ser	Gly	Pro	Asp	Arg	Glu	Arg	Arg	Glu	Thr	Thr	Pro		
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Ser	Ser	Arg	Ala	His	Gly	Glu	Leu	Ser	Asp	Leu	Glu	Ser	Asp	Leu	Ala		
		175					180					185					
ggg	cac	aag	act	ggc	ccg	tcg	cta	ccg	gcg	gca	acg	ccg	gct	gcg	gag		745
Gly	His	Lys	Thr	Gly	Pro	Ser	Leu	Pro	Ala	Ala	Thr	Pro	Ala	Ala	Glu		
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Leu	Ile	Val	Pro	Pro	Ala	His	Glu	Ile	Gln	Glu	Phe	Phe	Ala	Ala	Ala		
	205				210					215					220		
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Glu	Ala	Ala	Gln	Ala	Lys	Arg	Phe	Ala	Ser	Lys	Tyr	Asn	Phe	Asp	Phe		
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gtc	cgc	ggc	gtg	ccc	ctc	gac	gcc	ggc	ggc	cgg	ttc	gag	tgg	gcg	ccg		889
Val	Arg	Gly	Val	Pro	Leu	Asp	Ala	Gly	Gly	Arg	Phe	Glu	Trp	Ala	Pro		
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Val	Val	Ser	Ile														
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gaaagatctg	gtttgtctca	aaaaaaaaaa	aaaaaaaaaa	aaaaaaagg	cgccgcgtct												1302
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 <212> PRT  
 <213> zea mays

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 35 40 45  
 Arg Ala Pro Ala Gly Glu Pro Ala Ala Val Ser Ala Gly Gly Asp  
 50 55 60  
 Gly Gly Ser Cys Tyr Ile His Leu Arg Ser Arg Met Leu Phe Met Ala  
 65 70 75 80  
 Pro Pro Gln Pro Gln Pro Ser Val Asp Ser Val Pro Thr Pro Val Glu  
 85 90 95  
 Ala Ala Asp Gly Ala Ala Gly Gln Gln Gly Ala Ala Leu Ala Ala Gly  
 100 105 110  
 Leu Ser Arg Cys Ser Ser Thr Ala Ser Ser Val Asn Leu Gly Leu Gly  
 115 120 125  
 Gly Gln Arg Gly Ser His Thr Cys Arg Ser Tyr Asp Ala Ala Glu Ala  
 130 135 140  
 Gly Gly Asp His Val Leu Val Asp Val Ser Ala Ala Ser Asn Ser Gly  
 145 150 155 160  
 Ser Gly Pro Asp Arg Glu Arg Arg Glu Thr Thr Pro Ser Ser Arg Ala  
 165 170 175  
 His Gly Glu Leu Ser Asp Leu Glu Ser Asp Leu Ala Gly His Lys Thr  
 180 185 190  
 Gly Pro Ser Leu Pro Ala Ala Thr Pro Ala Ala Glu Leu Ile Val Pro  
 195 200 205  
 Pro Ala His Glu Ile Gln Glu Phe Phe Ala Ala Glu Ala Ala Gln  
 210 215 220  
 Ala Lys Arg Phe Ala Ser Lys Tyr Asn Phe Asp Phe Val Arg Gly Val  
 225 230 235 240  
 Pro Leu Asp Ala Gly Gly Arg Phe Glu Trp Ala Pro Val Val Ser Ile  
 245 250 255

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<220>  
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 tcgaaacctt agcttgccca gccctccgg gcc atg ggc aag tac atg cgc aag 174

	Met	Gly	Lys	Tyr	Met	Arg	Lys	
	1				5			
gcc aag gct tcc agc gag gtt gtc atc atg gat gtc gcc gcc gct ccg								222
Ala Lys Ala Ser Ser Glu Val Val Ile Met Asp Val Ala Ala Ala Pro								
	10				15		20	
ctc gga gtc cgc acc cga gcg cgc gcc ctc gcg ctg cag cgt ctg cag								270
Leu Gly Val Arg Thr Arg Ala Arg Ala Leu Ala Leu Gln Arg Leu Gln								
	25				30		35	
gag cag cag acg cag tgg gag gaa ggt gct ggc ggc gag tac ctg gag								318
Glu Gln Gln Thr Gln Trp Glu Glu Gly Ala Gly Gly Glu Tyr Leu Gln								
	40				45		50	55
cta agg aac cgg agg ctc gag aag ctg ccg ccg ccg ccg gcg acc acg								366
Leu Arg Asn Arg Arg Leu Glu Lys Leu Pro Pro Pro Pro Ala Thr Thr								
				60			65	70
agg agg tcg ggc ggg agg aaa gcg gca gcc gag gcc gcc gca act aag								414
Arg Arg Ser Gly Gly Arg Lys Ala Ala Ala Glu Ala Ala Ala Thr Lys								
				75			80	85
gag gct gag gcg tcg tac ggg gag aac atg ctc gag ttg gag gcc atg								462
Glu Ala Glu Ala Ser Tyr Gly Glu Asn Met Leu Glu Leu Glu Ala Met								
				90			95	100
gag agg att acc agg gag acg acg cct tgc agc ttg att aac acc cag								510
Glu Arg Ile Thr Arg Glu Thr Thr Pro Cys Ser Leu Ile Asn Thr Gln								
				105			110	115
atg act agc act cct ggg tcc acg aga tcc agc cac tct tgc cac cgc								558
Met Thr Ser Thr Pro Gly Ser Thr Arg Ser Ser His Ser Cys His Arg								
	120						125	130
agg gtg aac gct cct ccg gtg cac gcc gtc cca agt tcg agg gag atg								606
Arg Val Asn Ala Pro Pro Val His Ala Val Pro Ser Ser Arg Glu Met								
				140			145	150
aat gag tac ttc gct gcc gaa cag cga gcg caa caa cag gat ttc att								654
Asn Glu Tyr Phe Ala Ala Glu Gln Arg Arg Gln Gln Gln Asp Phe Ile								
				155			160	165
gac aag tac aac ttc gat cct gca aac gac tgc cct ctc cca ggc agg								702
Asp Lys Tyr Asn Phe Asp Pro Ala Asn Asp Cys Pro Leu Pro Gly Arg								
				170			175	180
ttt gag tgg gtg aag cta gac t gatggattca gagggacgag agagcagcag								754
Phe Glu Trp Val Lys Leu Asp								
	185						190	
gcatggaatg gaatggaact cccccccgc tccctccaca ccaccccgag gttgtggcag								814
aggcgcatag cgtcgtgtta gcttcgtttc tgctgtaaaa aaaaacttag tgttttagca								874
tgtagcctta attggtcgtg tgttacagta cagaactgat gctgagttac aacaccctga								934
tctggtcttg atctgatccc tcaactccaa tgtaaccctt aacagctcat tctgtaagga								994
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1089

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 <213> zea mays

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 35 40 45  
 Ala Gly Gly Glu Tyr Leu Glu Leu Arg Asn Arg Arg Leu Glu Lys Leu  
 50 55 60  
 Pro Pro Pro Pro Ala Thr Thr Arg Arg Ser Gly Gly Arg Lys Ala Ala  
 65 70 75 80  
 Ala Glu Ala Ala Ala Thr Lys Glu Ala Glu Ala Ser Tyr Gly Glu Asn  
 85 90 95  
 Met Leu Glu Leu Glu Ala Met Glu Arg Ile Thr Arg Glu Thr Thr Pro  
 100 105 110  
 Cys Ser Leu Ile Asn Thr Gln Met Thr Ser Thr Pro Gly Ser Thr Arg  
 115 120 125  
 Ser Ser His Ser Cys His Arg Arg Val Asn Ala Pro Pro Val His Ala  
 130 135 140  
 Val Pro Ser Ser Arg Glu Met Asn Glu Tyr Phe Ala Ala Glu Gln Arg  
 145 150 155 160  
 Arg Gln Gln Gln Asp Phe Ile Asp Lys Tyr Asn Phe Asp Pro Ala Asn  
 165 170 175  
 Asp Cys Pro Leu Pro Gly Arg Phe Glu Trp Val Lys Leu Asp  
 180 185 190

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<220>  
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 agcgagaaga aggcagtgtc gcggcgcgct tccgtaag atg ggg aag tac atg cgc 176  
 Met Gly Lys Tyr Met Arg  
 1 5  
 aag cgc agg ggg gcc gcg ggc gag ggg gtg gcc gca gtc gag gtc tcg 224  
 Lys Arg Arg Gly Ala Ala Gly Glu Gly Val Ala Ala Val Glu Val Ser  
 10 15 20  
 cag gtc gtc ggc gtc cgg acg agg tcc agg tcc gcg gcg gcg acc ggc 272  
 Gln Val Val Gly Val Arg Thr Arg Ser Arg Ser Ala Ala Ala Thr Gly  
 25 30 35

ggc ggt gtc gcg aag gtc gct ccg ccg agg agg aag aag gcg ctg ctg Gly Gly Val Ala Lys Val Ala Pro Pro Arg Arg Lys Lys Ala Leu Leu 40 45 50	320
ccc gcc gcg aac gtg acg acg tcg ggg gag cct ggt gcc gtg ggc gct Pro Ala Ala Asn Val Thr Thr Ser Gly Glu Pro Gly Ala Val Gly Ala 55 60 65 70	368
ggt ggt ggg gac ggc gga agc tgc tgc tac atc cac ctg cgg agc cgc Gly Gly Gly Asp Gly Gly Ser Cys Cys Tyr Ile His Leu Arg Ser Arg 75 80 85	416
atg ctg ttc atg gca gca cct cag cag caa ccg tcg gcg gct ctg acg Met Leu Phe Met Ala Ala Pro Gln Gln Gln Pro Ser Ala Ala Leu Thr 90 95 100	464
ccg gtg gag gct gct ggt gcg gca car caa ggc ggg gtg gtg gcg ctc Pro Val Glu Ala Ala Gly Ala Ala Xaa Gln Gly Gly Val Val Ala Leu 105 110 115	512
gcg gct ggc ctc tcg cgt tgc tcc agc acg gcg tcg tcg gtg gac gtc Ala Ala Gly Leu Ser Arg Cys Ser Ser Thr Ala Ser Ser Val Asp Val 120 125 130	560
ggg ggc cac gcc tgc cgc tcc gac gct gcg cct gcg gag gtt gac ggg Gly Gly His Ala Cys Arg Ser Asp Ala Ala Pro Ala Glu Val Asp Gly 135 140 145 150	608
gat cac gtc ccg gat gtc gtc acc gcg agc aac tcg ggg agc gtc ccg Asp His Val Pro Asp Val Val Thr Ala Ser Asn Ser Gly Ser Val Pro 155 160 165	656
gac cgc gag agg aga gag acg acg cca tcg tcg agc cgg gcg cac ggc Asp Arg Glu Arg Arg Glu Thr Thr Pro Ser Ser Ser Arg Ala His Gly 170 175 180	704
ggc gag ctc agc gat ctg gag tcg gat ctg gtg ggg cgg cag aag act Gly Glu Leu Ser Asp Leu Glu Ser Asp Leu Val Gly Arg Gln Lys Thr 185 190 195	752
ggc tgc tcg tcg tcg ccg gcg aca aca aca tcg gct gcg gag ctg atc Gly Cys Ser Ser Ser Pro Ala Thr Thr Thr Ser Ala Ala Glu Leu Ile 200 205 210	800
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 Ser Ala Ala Ala Thr Gly Gly Gly Val Ala Lys Val Ala Pro Pro Arg  
 35 40 45  
 Arg Lys Lys Ala Leu Leu Pro Ala Ala Asn Val Thr Thr Ser Gly Glu  
 50 55 60  
 Pro Gly Ala Val Gly Ala Gly Gly Gly Asp Gly Gly Ser Cys Cys Tyr  
 65 70 75 80  
 Ile His Leu Arg Ser Arg Met Leu Phe Met Ala Ala Pro Gln Gln Gln  
 85 90 95  
 Pro Ser Ala Ala Leu Thr Pro Val Glu Ala Ala Gly Ala Ala Xaa Gln  
 100 105 110  
 Gly Gly Val Val Ala Leu Ala Ala Gly Leu Ser Arg Cys Ser Ser Thr  
 115 120 125  
 Ala Ser Ser Val Asp Val Gly Gly His Ala Cys Arg Ser Asp Ala Ala  
 130 135 140  
 Pro Ala Glu Val Asp Gly Asp His Val Pro Asp Val Val Thr Ala Ser  
 145 150 155 160  
 Asn Ser Gly Ser Val Pro Asp Arg Glu Arg Arg Glu Thr Thr Pro Ser  
 165 170 175  
 Ser Ser Arg Ala His Gly Gly Glu Leu Ser Asp Leu Glu Ser Asp Leu  
 180 185 190  
 Val Gly Arg Gln Lys Thr Gly Cys Ser Ser Ser Pro Ala Thr Thr Thr  
 195 200 205  
 Ser Ala Ala Glu Leu Ile Val Pro Pro Ala Gln Glu Ile Gln Glu Phe  
 210 215 220  
 Phe Ala Ala  
 225

<210> 7  
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 <212> PRT  
 <213> zea mays

<400> 7  
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<210> 8  
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 <212> DNA  
 <213> zea mays

<220>  
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 <222> (1)...(21)  
 <223> n = Any nucleotide; r = nucleotide a or g; y = nucleotide t

or c

<400> 8  
atgggnaart ayatgcgnaa r

21

<210> 9  
<211> 21  
<212> DNA  
<213> zea mays

<220>  
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<223> n = Any nucleotide; r = nucleotide a or g; y = nucleotide t  
or c

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atgggnaart ayatgagraa r

21

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<212> PRT  
<213> zea mays

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Arg Phe Glu Trp Ala Pro Val Val Ser Ile  
35 40

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<212> PRT  
<213> zea mays

<400> 11  
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Glu Trp Val Lys Leu Asp  
35

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<212> PRT  
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<400> 12



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			20					25					30		
Leu	Asp	Ala	Gly	Arg	Phe	Glu	Trp	Thr	Pro	Gly	Val	Ser	Ile		
	35						40					45			